SEQUENCE LISTING

<110> Yen-Potin, Frances
      Denison, Blake
      Bour, Barbara
      Bihain, Bernard
      Dumas Milne Edwards, Jean-Baptiste
      Duclert, Aymeric
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14

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19

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21

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27

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28

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<213> Homo sapiens

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<222> 30..1121

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ctg gct ctt ctt tca gcg ttt tcg gcc acc cag gca cgg aaa ggc ttc        101
Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe
        15                  20                  25
tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag        149
Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln
        30                  35                  40
atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc        197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser
        45                  50                  55
ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg        245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg
60                  65                  70                  75
cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac ccg gtg ggc        293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly
                80                  85                  90
atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc        341
Met Arg Arg Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu
                95                  100                 105
cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag        389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu
        110                 115                 120
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29

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ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag          437
Gly Leu Arg Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln
    125                 130                 135
gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg          485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly
140                 145                 150                 155
gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct          533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala
                160                 165                 170
ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc          581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe
                175                 180                 185
aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg          629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly
            190                 195                 200
cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc          677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala
    205                 210                 215
agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc          725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu
220                 225                 230                 235
acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac          773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp
                240                 245                 250
cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag          821
Gln Leu Arg Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu
                255                 260                 265
gaa ggg gcc ggc ccg gac ccc cag atg ctc tcc gag gag gtg cgc cag          869
Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln
            270                 275                 280
cga ctt cag gct ttc cgc cag gac acc tac ctg cag ata gct gcc ttc          917
Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe
    285                 290                 295
act cgc gcc atc gac cag gag act gag gag gtc cag cag cag ctg gcg          965
Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala
300                 305                 310                 315
cca cct cca cca ggc cac agt gcc ttc gcc cca gag ttt caa caa aca         1013
Pro Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr
                320                 325                 330
gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg         1061
Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu
            335                 340                 345
tgg gaa gac atc act cac agc ctt cat gac cag ggc cac agc cat ctg         1109
Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu
    350                 355                 360
ggg gac ccc tga ggatctacct gcccaggccc attcccagct cyttgtctgg            1161
Gly Asp Pro  *
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30

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gcccatgttt cctgacatag ctctacacct aaataaggga ctgaaccctc ccaactgtgg    1761
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Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
        35                  40                  45
Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
    50                  55                  60
Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser
65                  70                  75                  80
Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu
            85                  90                  95
Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala
        100                 105                 110
Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
        115                 120                 125
Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val
    130                 135                 140
Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala
145                 150                 155                 160
Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu
            165                 170                 175
Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His
            180                 185                 190
Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu
    195                 200                 205
Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu
    210                 215                 220
Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys
225                 230                 235                 240
Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu
            245                 250                 255
Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro
            260                 265                 270
Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe
    275                 280                 285
Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp
    290                 295                 300
Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly
305                 310                 315                 320
His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val
            325                 330                 335
Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr
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His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro
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31
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<223> 3'regulatory        region

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<220>
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<222> 3213
<223> 17-41-250    : polymorphic base C or T

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<220>
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33

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